ABSTRACT

The present invention provides methods for determining the genotype of a selected gene present in at least two alleles in a sample. The methods involve amplifying DNA from the sample with a first pair of flanking primers that hybridize to nucleic acid sequences flanking a variant-specific gene sequence, the presence of which indicates the presence of a first gene variant, and the absence of which indicates the presence of a second gene variant. The DNA is also amplified with a third primer that specifically binds to the variant-specific sequence and together with one of the flanking primers forms a second pair of primers. Detection of one or more nucleic acid products of the amplification reaction is indicative of the genotype present in the sample.